



## SEQUENCE LISTING

<110> Junghans, Richard P.

<120> Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen

<130> 002

<140> 10/006,771

<141> 2001-12-10

<150> 60/250,090

<151> 2000-11-30

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 7654

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2428)..(3759)

<223> Chimeric IgTCR sequence contained in retroviral vector. Retroviral vector sequence (non-coding regions) are incidental to the invention. The translated (coding region) is relevant to the invention. (pertinent to Figure 3.)

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gaaagcccag gctgggagcc cagcagtttg catcccctcc tggcgtgtac ctaagggttt 240

cttaattgtg tggtttctaa atcttccaga gggtttgtct cattcacttc cacttcgggtg 300

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tgaacctgag gcccaattct tcagcttggt aaggagagca caagcaccag aagaggctga 420

cccggcagac ctgtgggcat ttttaacaag ggctcctgg gtctgtggga ggcaggctta 480

cataaggtgc aaattagaaa tataaataat aagcccatat caatttgtca tcttttttta	540
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Leu Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln
10                      15                      20                      25

agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc 2550
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
30                      35                      40

tgt aag gcc agt cag gat gtg ggt act tct gta gct tgg tac cag cag 2598
Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln
45                      50                      55

aag cca ggt aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg 2646
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg
60                      65                      70

cac act ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac 2694
His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
75                      80                      85

ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gcc acc tac 2742
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr
90                      95                      100                      105

tac tgc cag caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag 2790
Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys
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Gly Ser Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val	
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Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp	
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Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly	
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Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr	
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Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly	
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Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr	
250 255 260 265	
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Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln	
270 275 280	
ccc ctg tcc ctg cgc cca gag gcg gct cgg cca gcg gcg ggg ggc gca	3318
Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala	
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gtg cac acg agg ggg ctg gac ttc gcc ctg gat ccc aaa ctc tgc tac	3366
Val His Thr Arg Gly Leu Asp Phe Ala Leu Asp Pro Lys Leu Cys Tyr	
300 305 310	

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Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu	
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ttc ctg aga gtg aag ttc agc agg agc gca gag ccc ccc gcg tac cag	3462
Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln	
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Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu	
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gag tac gat gtt ttg gac aag aga cgt ggc cgg gac cct gag atg ggg	3558
Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	
365 370 375	
gga aag ccg aga agg aag aac cct cag gaa ggc ctg tac aat gaa ctg	3606
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu	
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Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly	
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Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser	
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Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro	
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<213> Homo sapiens

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Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
          20           25           30

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Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
          35           40           45

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Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
50           55           60

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Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg

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65		70		75		80
Phe Ser Gly Ser	Gly Ser Gly Thr Asp	Phe Thr Phe Thr Ile Ser Ser	85	90	95	
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu			100	105	110	
Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly			115	120	125	
Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Glu Val Gln			130	135	140	
Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg			145	150	155	160
Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser			165	170	175	
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile			180	185	190	
His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg			195	200	205	
Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met			210	215	220	
Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu			225	230	235	240
Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val			245	250	255	
Thr Val Ser Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro						

260	265	270
Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu		
275	280	285
Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp		
290	295	300
Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe		
305	310	315
Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser		
325	330	335
Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr		
340	345	350
Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys		
355	360	365
Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn		
370	375	380
Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu		
385	390	395
Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly		
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His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr		
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Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		
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<211> 422
<212> DNA
<213> Homo sapiens and Mus sp.

<220>
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<222> (8)..(421)
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      region (aa20-138) with leader (aa1-19) (pertinent to Fig. 4A.)

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      Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala
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aca ggt gtc cac tcc gag gtc caa ctg gtg gag agc ggt gga ggt gtt      97
Thr Gly Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val
15                    20                    25                    30

gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc      145
Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe
                    35                    40                    45

gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa      193
Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys
                    50                    55                    60

ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac      241
Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn
65                    70                    75

tat gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc      289
Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala
80                    85                    90

aag aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc      337
Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr
95                    100                    105                    110

ggg gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct      385
Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala
115                    120                    125

tat tgg ggc caa ggg acc ccg gtc acc gtc tcc tca g      422
Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser
130                    135

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 <212> PRT  
 <213> Homo sapiens and Mus sp.

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Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln  
 20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe  
 35 40 45

Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala  
 65 70 75 80

Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 85 90 95

Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val  
 100 105 110

Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp  
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Gly Gln Gly Thr Pro Val Thr Val Ser Ser  
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<210> 5  
 <211> 712  
 <212> DNA  
 <213> Homo sapiens and Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (14)..(712)

<223> hMN14 VLCK, humanized (CDR-grafted) anti-CEA antibody kappa light chain V region (aa20-126), with human constant CK domain (aa127-232) and leader (aa1-19). (pertinent to Figure 4B.)

&lt;400&gt; 5

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala	
1 5 10	
aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag agc cca agc	97
Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser	
15 20 25	
agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aag gcc	145
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala	
30 35 40	
agt cag gat gtg ggt act tct gta gct tgg tac cag cag aag cca ggt	193
Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly	
45 50 55 60	
aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg cac act ggt	241
Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly	
65 70 75	
gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc	289
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe	
80 85 90	
acc atc agc agc ctc cag cca gag gac atc gcc acc tac tac tgc cag	337
Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln	
95 100 105	
caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag gtg gaa atc	385
Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile	
110 115 120	
aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat	433
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
125 130 135 140	
gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac	481
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn	

	145	150	155	
ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc				529
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu				
	160	165	170	
caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac				577
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp				
	175	180	185	
agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac				625
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr				
	190	195	200	
gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc				673
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser				
	205	210	215	220
tcg ccc gtc aca aag agc ttc aac agg gga gag tgt taa				712
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys				
	225	230		

<210> 6  
 <211> 232  
 <212> PRT  
 <213> Homo sapiens and Mus sp.

<400> 6

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15
Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala			
	20	25	30
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val			
	35	40	45
Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys			
	50	55	60
Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg			
	65	70	75
			80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu  
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val  
115 120 125

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
130 135 140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
145 150 155 160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
165 170 175

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
180 185 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
195 200 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
210 215 220

Lys Ser Phe Asn Arg Gly Glu Cys  
225 230